

(Original aus
OEB: 9.10.97)

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Rotkreuzstiftung Zentrallaboratorium
Blutspendedienst
- (B) STREET: Wankdorfstrasse 10
- (C) CITY: Bern 22
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): CH-3000

(ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity
against Rhesus D antigens, DNA encoding them, complete
antibodies comprising the Fab fragments and process for
their preparation

(iii) NUMBER OF SEQUENCES: 64

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/EP97/03253

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 96810421.6
- (B) FILING DATE: 24-JUN-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD1
- (B) CLONE: LD1-40

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION:join(91..105, 148..198, 295..342)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..375
(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 1ln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg	48
1 5 10 15	
CC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr	96
20 25 30	
CC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
35 40 45	
CA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val	192
50 55 60	
AGG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	240
65 70 75 80	
CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys	288
85 90 95	
GCG AGA GAG CGA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met	336
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro	375
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15	
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30	
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	

la Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60

ys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

eu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

la Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
 100 105 110

sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro
 115 120 125

2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-40

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

TC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT
'al Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
20 25 30

4
96

GG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
35 40 45

144

CG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

192

CT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
65 70 75 80

240

TTT GCA ACT TAC TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
85 90 95

288

TC GGC CAA GGG ACA CGA CTG GAG ACT AAA
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys
100 105

318

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
(D) DEVELOPMENTAL STAGE: Adult
(E) HAPLOTYPE: diploid
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD1
(B) CLONE: LD1-52

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: Chromosome 14
(B) MAP POSITION: q32.3
(C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..375
(D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG ;ln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly	48
1 5 10 15	
TCCT CGC AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser	96
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG ;ly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	144
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	192
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	240
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	288
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	336
100 105 110	

AC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA
 Isp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

7
(A) LIBRARY: cDNA Library, LD1
(B) CLONE: LD1-52

(viii) POSITION IN GENOME:
(A) CHROMOSOME SEGMENT: Chromosome 2
(B) MAP POSITION: P 11
(C) UNITS: chromosome b.No

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..318
(D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:
(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	48
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn	96
20 25 30	
GGG TAT CAG CAG AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly	144
35 40 45	
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	192
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT AGT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	240
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC CGT ACC CCT CCA TTC ACT Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Arg Thr Pro Pro Phe Thr	288
85 90 95	
TTC GGC CCT GGG ACC AAA GTG GAG ATC AAA Phe Gly Pro Gly Thr Lys Val Glu Ile Lys	318
100 105	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 20 25 30	

rp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
35 40 45

la Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

er Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
85 90 95

he Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-84

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

CC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT er Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 20 25 30	96
GC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG ly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
CA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG la Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60	192
AG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT ys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80	240
TC CAA ATG CGC AGT CTG AGT GCC GAC GAC GCT GTG TAT TAC TGT eu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
CG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG la Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110	336
AC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	375

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 11:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-84

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn	
20 25 30	
TGG TAT CAG CAC AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT	144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala	
35 40 45	
GCA TCG AAT TTG CAA ACT GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA	192
Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT GAC CTG CAG CCT GAG GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp	
65 70 75 80	
TTC GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT AGG CCG TTC ACT TTT	288

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

GC CGG GGG ACC AGC CTG GAC ATC AAA
ly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

315

2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala
35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
(D) DEVELOPMENTAL STAGE: adult
(E) HAPLOTYPE: diploid
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA LIBRARY, LD1

(B) CLONE: LD1-110

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..348)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT	96
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr	
20 25 30	
GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA GGT ATA TGG TTT GAT GGA AGC AAC AAA AAC TAT GCA GAC TCC GTG	192
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC TCC AAG AAC ACT CTG TTT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe	
65 70 75 80	
CTG CAC ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT ACA TAT TAC TGT	288
Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys	
85 90 95	
GCG AGA GAG AGG GCG ATT CGG GGA ATC AGT AGA TAC AAT TAC TAC ATG	336
Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: Diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA Library, LD1
 - (B) CLONE: LD1-110
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: chromosome b.No
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn	
20 25 30	
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala	
35 40 45	
GCA TCC AGT TTG CAA AGT GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly	
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAG CCT GAA GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC AGT TCC TCG TGG ACG TTC	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe	
85 90 95	
GGC CAA GGG ACC AAG GTG GAA ATC AAA	315
Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn	
20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala	
35 40 45	
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly	
50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe	
85 90 95	
Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
- (B) CLONE: LD1-117

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(x) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG	GTG	AAA	CTG	CTC	GAG	TCA	GGA	GGA	GGC	GTG	GTC	CAG	CCT	GGG	AAG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Lys	
1			5						10			15				
TCC	CTG	AGA	CTT	TCC	TGT	GCA	GCG	TCT	GGA	TTC	AGT	TTC	AAT	AGC	CAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Asn	Ser	His	
20						25						30				
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35						40					45					
GCA	TTT	ATA	TGG	TTT	GAT	GGC	AGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
50						55			60							
AAG	GGC	CGA	TTC	ACC	ATC	ACC	AGA	GAC	AAC	TCC	AAG	AAC	ACG	CTG	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Thr	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65						70			75			80				
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCT	GTC	TAT	TAC	TGT	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	

85

90

95

336

CG AGA GAG ACC TCA GTA AGG CTA GGG TAT AGC CGC TAC AAT TAC TAC
 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
 100 105 110

378

TG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC ATC TCG TCA
 Ile Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
 100 105 110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor

13

- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD1
 - (B) CLONE: LD1-117

- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn	
20 25 30	
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
GCA TCC AGT TTG CAA GGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA	192
Ala Ser Ser Leu Gln Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC AGG GCC CCT CAG TGG ACG	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr	
85 90 95	
TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA	318
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD2
 - (B) CLONE: LD2-1
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..375
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (x) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	48
TCG CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30	96
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60	192
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80	240
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110	336
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	375

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95

20
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD2
- (B) CLONE: LD2-1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 22
- (B) MAP POSITION: q11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..333
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(x) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(61..99, 145..165, 262..294)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
1 5 10 15

48

ACC ATC TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val
20 25 30

96

TAC TGG TAC CAG AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
35 40 45

144

AAG AAT GAT CAG CGG CCC TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser

192

50	55	60	
AAG TCT GGC ACC TCG GCC TCC CTG GCC ATC AGT GGG CTC CGG TCC GAG			240
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu			
65	70	75	80
GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC			288
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly			
85	90	95	
CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC			333
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro			
100	105	110	

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val			
1	5	10	15
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val			
20	25	30	
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr			
35	40	45	
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser			
50	55	60	
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu			
65	70	75	80
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly			
85	90	95	
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro			
100	105	110	

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homo sapiens

22

(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA Library, LD2
 (B) CLONE: LD2-4

(viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: chromosome 14
 (B) MAP POSITION: q32.3
 (C) UNITS: Chromosome band number

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..375
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:
 (A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG	192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG	336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION:join(64..96, 142..162, 259..282)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	48
1 5 10 15	
TG ACC ATC ACT TGC CGG ACA AGT CAG ACC ATT AGC AGA AAT TTA AAT Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn	96
20 25 30	
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	144
35 40 45	
ACA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	192
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AAT AGT CTA CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp	240
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCT TCG TTC GGC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Pro Ser Phe Gly	288
85 90 95	
CAA GGG ACC AAG GTG GAA ATC AAA Gln Gly Thr Lys Val Glu Ile Lys	312
100	

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15	
Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45	
Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Pro Ser Phe Gly	

Gln Gly Thr Lys Val Glu Ile Lys
100

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD2
 (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: chromosome 2
 (B) MAP POSITION: p11
 (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..375
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG
 Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

48

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

96

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

144

GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

192

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG CTC TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr 65 70 75 80	240
CTG CAA ATG AAT AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110	336
GAC GTC TGG GGC AAG GGG GCC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 115 120 125	375

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly 1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr 65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CDND library. LD2
- (B) CLONE: LD2-5

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn	
20 25 30	
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala	
35 40 45	
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
TCT GGG ACA GAT TTC ACC CTC ACC ATC AGC AGT CTG CAA CCT GAG GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GGA ACT TAC TAC TGT CAA CAG AAT TAC AGG ACC CCT CAG TGG ACG	288
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr	
85 90 95	
TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA	318
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid

28
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
35 40 45
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-10

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION:join(91..105, 148..198, 298..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	48
TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30	96
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60	192
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 175 180 185	240
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TAT Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr 85 90 95	288
TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr 100 105 110	336
CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	378

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80

leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
 85 90 95

lys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
 100 105 110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-10
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME SEGMENT: chromosome 22
 - (B) MAP POSITION: q11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..333
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (x) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(61..102, 148..168, 265..294)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC
 Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
 1 5 10 15

48

ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT
 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr
 20 25 30

96

CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT
 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile
 35 40 45

144

31
TAT AGT ACA AAC AAA AAA CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
50 55 60

192

TCC CTC CTT GGG GGC AAA GCT GCC CTG ACA CTG TCA GGT GTG CAG CCT
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
65 70 75 80

240

GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC TAC TAT GGT GGT GCT CAA
Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Gly Gly Ala Gln
85 90 95

288

CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC
Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro
100 105 110

333

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
1 5 10 15

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr
20 25 30

Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile
35 40 45

Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
50 55 60

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
65 70 75 80

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln
85 90 95

Leu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG	192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG	336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: lymphocyte

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD2
 (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: chromosome 2
 (B) MAP POSITION: p11
 (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..315
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA	48
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn	
20 25 30	
TGG TAT CAG CAC AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT	144
Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
GTA TCC GCT TTG CAA AGT GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA	192
Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg	
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT CCC CCG TAC ACT TTC	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe	
85 90 95	
GGC CAG GGG ACC AAC CTG CAG ATC AAA	315
Gly Gln Gly Thr Asn Leu Gln Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn	
20 25 30	
Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg	
50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD2
 (B) CLONE: LD2-14

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: chromosome 14
 (B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..375
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

48

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

96

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

144

GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT

192

36

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val	50	55	60	
AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT	65	70	75	240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr				
CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT	85	90	95	288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys				
GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG	100	105	110	336
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met				
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA	115	120	125	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser				

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	1	5	10	15
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe	20	25	30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val	50	55	60	
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75	80
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95	
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	100	105	110	
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	115	120	125	

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: lymphocyte

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-14

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn	
20 25 30	
TGG TAT CAG CAG AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala	
35 40 45	
GCA TCC AGT TTG CAA AGT GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly	
50 55 60	
TCT GGG AGA GAT TTC ACT CTC ACC GTC ACC AGT CTG CAA CCT GAA GAT	240
Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG TGG ACG TTC	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe	
85 90 95	
GGC CAA GGG ACC AAG GTG GAA ATC AAA	315
Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
 50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library
 (B) CLONE: LD2-17

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: chromosome 14
 (B) MAP POSITION: q32.43
 (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..375

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

39

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT	96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG	192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT	288
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG	336
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu	
100 105 110	
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr	
20 25 30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val	
50 55 60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-17
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA
 Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

48

GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT
 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
 20 25 30

96

41

TGG TAT CAG CAG AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45	144
GCA TCC AGG TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60	192
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC ACT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80	240
TTT GCG ACT TAC TAC TGT CAA CAG AGT TAC AGT GCC CCT TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95	288
GGC CAA GGG ACC AAG CTG GAA ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105	315

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95
Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library LD2
- (B) CLONE: LD2-20

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1			5						10					15		
TCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TCC	AGG	AGT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Ser	Arg	Ser	Tyr	
20						25						30				
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
50						55				60						
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
65					70				75			80				
AAG	GGC	CGA	TTC	ACC	ATC	TCC	CGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
85								90			95					
CTG	CAA	ATG	AAG	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Lys	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
100						105					110					
GCG	AGA	GAG	AAG	GCG	CTT	CGG	GGG	ATC	AGT	AGA	TAC	AAC	TAT	TAC	CTG	336
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu	
205						210				215						
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
115					120				125							

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-20

(viii) POSITION IN GENOME:

44

(A) CHROMOSOME SEGMENT: chromosome 2
 (B) MAP POSITION: p11
 (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..315
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	48
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn	96
20 25 30	
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	144
35 40 45	
GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	192
50 55 60	
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	240
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CGA TTC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe	288
85 90 95	
GGC CCT GGG ACC AAA GTG GAT ATC AAA Gly Pro Gly Thr Lys Val Asp Ile Lys	315
100 105	

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45	

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
85 90 95

Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(x) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..351)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

48

TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

96

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

GCA GAT ATA TGG TTT GAT GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG
 Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
 50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTG TAT TAC TGT
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA CTC CAC TAC TAC
 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110

TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA
 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 220 225 230

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(x) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr	
20 25 30	
TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
GCA TCC AAT TTA CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA	192
Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
TCT GGC ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAT TAC TGT CTA CAA GAT AAC AAT TTC CCG TAC ACT TTT	288
Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe	
85 90 95	

48
 GGC CAG GGG ACC AAG CTG GAG ATC AAA
 Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe
 85 90 95
 Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD1 and LD2
 (B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

(A) CHROMOSOME SEGMENT: chromosome 14
 (B) MAP POSITION: q32.3
 (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..375
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5						10				15		
TCC	CTG	AGA	GTC	GCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AAT	TTT	96
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe	
20						25							30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
35						40					45					
GCT	TTT	ATT	TGG	TTT	GAT	GCA	AGT	AAT	AAA	GGA	TAT	GGA	GAC	TCC	GTT	192
Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Tyr	Asp	Ser	Val
50					55					60						
AAG	GGC	CGA	TTC	ACC	GTC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75				80		
CTG	CAA	ATG	AAC	GGC	CTG	AGA	GCC	GAA	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
85						90					95					
GCG	AGA	GAG	AAG	GCG	GTT	CGG	GGG	ATT	AGT	AGA	TAC	AAC	TAC	TAC	ATG	336
Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
100						105					110					
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
115					120					125						

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10		15				
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe
20						25					30				

:ly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(x) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

48

GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

96

GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

144

TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
 35 40 45

192

GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60

240

TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

288

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
 85 90 95

315

GGC CAG GGG ACC AAG CTG CAG ATC AAA
 Gly Gln Gly Thr Lys Leu Gln Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs

52

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-2-33

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1										10				15		
RCC	CTG	AGA	GTC	GCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AAT	TTT	96
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe	
										20	25		30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
										35	40		45			
GCT	TTT	ATT	TGG	TTT	GAT	GCA	AGT	AAT	AAA	GGA	TAT	GGA	GAC	TCC	GTT	192
Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val	
										50	55		60			
AAG	GGC	CGA	TTC	ACC	GTC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
										65	70		75		80	
CTG	CAA	ATG	AAC	GGC	CTG	AGA	GCC	GAA	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
										85	90		95			

CG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG
la Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

336

AC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA
sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

375

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor
(D) DEVELOPMENTAL STAGE: adult
(E) HAPLOTYPE: diploid

54

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-6-33

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA	48
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
TC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn	
20 25 30	
GG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT	144
Irp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala	
35 40 45	
CA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA	192
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val	
50 55 60	
CT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Pro Tyr Thr Phe	
85 90 95	
GC CAG GGG ACC AAG CTG CAG ATC AAA	315
Gly Gln Gly Thr Lys Leu Gln Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	

55

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
100 105